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AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 1
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RDSEGEVLRKTAHRVDLJAKYJGGLRECEKRJKCLESCANYCMLLLSSMTDTLAPGGTYSSSQNCGCRSQPASARDREYLESGLPPSDT

Figure 2
(Sheet 2 of 17)
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Human TRFt nucleotide sequenc
SEQ New: 3498 bp;
Composition: 634 A; 1089 C; 1143 G; 632 T; 0 OTHER
Percentage: 18% A; 31% C; 33% G; 18% T; 0%OTHER

Molecular Weight (kDa): ssDNA: 1081.34   dsDNA: 2157.

ORIGIN

```
  :    ATGCAGGATG TCCAAGGCCC CCGTCCCGGA AGCCCCGGGG ATGCTGAAGA CCGGCGGGAC
 6:    CTGGGCTTGC ACAGGGGCGA GGTCAACTTT GGAGGGTCTG GGAAGAAGCG AGGCAAGTTT
 12:   GTACGGGTGC CGAGCGGAGT GGCCCCGTCT GTGCTCTTTG ACCTGCTGCT TGCTGAGTGG
 18:   CACCTGCCGG CCCCCAACCT GGTGGTGTCC CTGGTGGGTG AGGAGCAGCC TTTCGCCATG
 24:   AAGTCCTGGC TGCGGGATGT GCTGCGCAAG GGGCTGGTGA AGGCGGCTCA GAGCACAGGA
 30:   GCCTGGATCC TGACCAGTGC CCTCCGCGTG GGCCTGGCCA GGCATGTCGG GCAGGCCGTG
 36:   CGCGACCACT CGCTGGCCAG CACGTCCACC AAGGTCCGTG TGGTTGCTGT CGGCATGGCC
 42:   TCGCTGGGCC GCGTCCTGCA CCGCCGCATT CTGGAGGAGG CCCAGGAGGA TTTTCCTGTC
 48:   CACTACCCTG AGGATGACGG CGGCAGCCAG GGCCCCCTCT GTTCACTGGA CAGCAACCTC
 54:   TCCCACTTCA TCCTGGTGGA GCCAGGCCCC CCGGGGAAGG GCGATGGGCT GACGGAGCTG
 60:   CGGCTGAGGC TGGAGAAGCA CATCTCGGAG CAGAGGGCGG CTACGGGGG CACTGGCAGC
 66:   ATCGAGATCC CTGTCCTCTG CTTGCTGGTC AATGGTGATC CCAACACCTT GGAGAGGATC
 72:   TCCAGGGCCG TGGAGCAGGC TGCCCCGTGG CTGATCCTGG TAGGCTCGGG GGGCATCGCC
 78:   GATGTGCTTG CTGCCCTAGT GAACCAGCCC CACCTCCTGG TGCCCAAGGT GGCCGAGAAG
 84:   CAGTTTAAGG AGAAGTTCCC CAGCAAGCAT TTCTCTTGGG AGGACATCGT GCGCTGGACC
 90:   AAGCTGCTGC AGAACATCAC CTCACACCAG CACCTGCTCA CCGTGTATGA CTTCGAGCAG
 96:   GAGGGCTCCG AGGAGCTGGA CACGGTCATC CTGAAGGCGC TGGTGAAAGC CTGCAAGAGC
102:   CACAGCCAGG AGCCTCAGGA CTATCTGGAT GAGCTCAAGC TGGCCGTGGC CTGGGACCGC
108:   GTGGACATCG CCAAGAGTGA GATCTTCAAT GGGGACGTGG AGTGGAAGTC CTGTGACCTG
114:   GAGGAGGTGA TGGTGGACGC CCTGGTCAGC AACAAGCCCG AGTTTGTGCG CCTCTTTGTG
120:   GACAACGGCG CAGACGTGGC CGACTTCCTG ACGTATGGGC GGCTGCAGGA GCTCTACCGC
126:   TCCGTGTCAC GCAAGAGCCT GCTCTTCGAC CTGCTGCAGC GGAAGCAGGA GGAGGCCCGG
132:   CTGACGCTGG CCGGCCTGGG CACCCAGCAG GCCCGGGAGC CACCCGCGGG GCCACCGGCC
138:   TTCTCCCTGC ACGGCCGGCC AGGGGACCGC AGGAGGGCGG AGAAGGGCCC GGCCAAGCGC
144:   TTCTACCAGG ACGGCCGGCC AGGGGACCGC AGGAGGGCGG AGAAGGGCCC GGCCAAGCGC
150:   CCCACGGGCC AGAAGTGGCT GCTGGACCTG AACCAGAAGA GCGAGAACCC CTGGCGGGAC
156:   CTGTTCCTGT GGGCCGTGCT GCAGAACCGC CACGAGATGG CCACCTACTT CTGGGCCATG
162:   GGCCAGGAAG GTGTGGCAGC CGCACTGGCC GCCTGCAAAA TCCTCAAAGA GATGTCGCAC
168:   CTGGAGACGG AGGCCGAGGC GGCCCGAGCC ACGCGCGAGG CGAAATACGA GCGGCTGGCC
174:   CTTGACCTCT TCTCCGAGTG CTACAGCAAC AGTGAGGCCC GCGCCTTCGC CCTGCTGGTG
180:   CGCCGGAACC GCTGCTGGAG CAAGACCACC TGCCTGCACC TGGCCACCGA GGCTGACGCC
186:   AAGGCCTTCT TTGCCCACGA CGGCGTTCAG GCCTTCCTGA CCAGGATCTG GTGGGGGGAC
192:   ATGGCCGCAG GCACGCCCAT CCTGCGGCTG CTAGGAGCCT CCTCTGCCC CGCCCTCGTC
198:   TATACCAACC TCATCACCTT CAGTGAGGAA GCTCCCCTGA GGACAGGCCT GGAGGACCTG
204:   CAGGACCTGG ACAGCTGGA CACGGAGAAG AGCCGCTGT ATGGCCTGCA GAGCCGGGTG
210:   GAGGAGCTGG TGGAGGCGCC GAGGGCTCAG GGTGACCGAG GCCCACGTGC TGTCTTCCTG
216:   CTCACACGCT GGCGGAAATT CTGGGGCGCT CCCGTGACTG TGTTCCTGGG GAACGTGGTC
222:   ATGTACTTCG CCTTCCTCTT CCTGTTCACC TACGTCCTGC TGGTGGACTT CAGGCCGCCC
228:   CCCCAGGGCC CCTCAGGGCC CGAGGTCACC CTCTACTTCT GGGTCTTTAC GCTGGTGCTG
234:   GAGGAAATCC GGCAGGCTT CTTCACAGAC GAGGACACAC ACCTGGTGAA GAAGTTCACA
240:   CTGTATGTGG GGGACAACTG GAACAAGTGT GACATGGTGG CCATCTTCCT GTTCATCGTG
246:   GGTGTCACCT GCAGGATGCT GCCGTCGGCG TTTGAGGCTG GCCGCACGGT CCTCGCCATG
252:   GAGTTCATGG TGTTCACGCT GCGGCTGATC CATATCTTTG CCATACACAA GCAGCTGGGC
258:   CCCAAGATCA TCGTGGTAGA GCGCATGATG AAGGACGTCT TCTTCTTCCT CTTCTTTCTG
264:   AGCGTGTGGC TCGTGGCCTA CGGTGTCACC ACCCAGGCGC TGCTGCACCC CCATGACGGC
270:   CGCCTGGAGT GGATCTTCCG CCGGGTGCTC TACCGGCCCT ACCTGCAGAT CTTCGGCCAG
276:   ATCCCACTGG ACGAGATTGA TGAAGCCCGT GTGAACTGCT CCACCCACCC ACTGCTGCTG
282:   GAGGACTCAC CATCCTGCCC CAGCCTCTAT GCCAACTGGC TGGTCATCCT CCTGCTGGTC
288:   ACCTTCCTGT TGGTGAACAA TGTGGTGCTG ATGAACCTGC TCATCGCCAT GTTCAGCTAC
294:   ACGTTCCAGG TGGTGCAGGG CAACGCAGAC ATGTTCTGGA AGTTCCAGCG CTACAACCTG
```

Figure 3A
(Sheet 3 of 17)
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```
301.   ATTGTGGAGT ACCACGAGCG CCCCGCCCTG GCCCCGCCCT TCATCCTGCT CAGCCACCTG
301.   AGCCTGACGC TCCGCCGGGT CTTCAAGAAG GAGCCTGAGC ACAAGCGGGA GCACCTGGAG
311.   AGAGACCTGC CAGACCCCCT GGACCAGAAG GTCGTCACCT GGGAGACAGT CCAGAAGGAG
331.   AACTTCCTGA GCAAGATGGA GAAGCGGAGG AGGCACAGCG AGGGGGAGGT GCTGCGGAAA
324.   ACCGCCCACA GAGTGGACTT CATTGCCAAG TACCTCGGGG GGCTGAGAGA GCAAGAAAAG
331.   CGCATCAAGT GTCTGGAGTC ACAGATCAAC TACTGCTCGG TGCTCGTGTC CTCCGTGGCT
331.   GACGTGCTGG CCCAGGGTGG CGGCCCCCGG AGCTCTCACC ACTGTGGCGA GGGAAGCCAG
341.   CTGGTGGCTG CTGACCACAG AGGTGGTTTA GATGGCTGGG AACAACCCGG GGCTGGCCAG
341.   CCTCCCTCGG ACACATGA
```

Figure 3B
(sheet 4 of 17)
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ORIGIN

```
        MODVQGFRPG SPGDAEDRRE LGLHRGEVNF GGSGKKRGKF VRVPSGVAPS
 1      VLFDLLLAEW HLFAFNLVVS LVGEEQFFAM KSWLRDVLRK GLVKAAQSTG
 10     AWILTSALRV GLARHVGQAV RDHSLASTST KVRVVAVGMA SLGRVLHRR·
 1      LEEAQEDFPV HYFEDDGGSQ GFLCSLDSNL SHFILVEPGP PGKGDGLTEL
 20     RLRLEKHISE QRAGYGGTGS IEIFVLCLLV NGDPNTLERI SRAVEQAAPK
 25     LILVGSGGIA DVLAALVNQF HLLVPKVAEK QFKEKFPSKH FSWEDIVRW1
 30     KLLQNITSHQ HLLTVYDFEQ EGSEELDTVI LKALVKACKS HSQEPQDYLI·
 35     ELKLAVAWDR VDIAKSEIFN GDVEWKSCDL EEVMVDALVS NKPEFVRLFV
 40     DNGADVADFL TYGRLQELYR SVSRKSLLFD LLQRKQEEAR LTLAGLGTQQ
 45     AREFFAGFPA FSLHEVSRVL KDFLQDACRG FYQDGRPGDR RRAEKGPAKF
 50     FTGQKWLLDL NQKSENFWRD LFLWAVLQNR HEMATYFWAM GQEGVAAALA
 55     ACKILKEMSH LETEAEAARA TREAKYERLA LDLFSECYSN SEARAFALLV
 60     RRNRCWSKTT CLHLATEADA KAFFAHDGVQ AFLTRIWWGD MAAGTPILRL·
 65     LGAFLCFALV YTNLITFSEE AFLRTGLEDL QDLDSLDTEK SPLYGLQSRV·
 70     EELVEAPRAQ GDRGPRAVFL LTRWRKFWGA PVTVFLGNVV MYFAFLFLF1
 75     YVLLVDFRPP PQGPSGFEVT LYFWVFTLVL EEIRQGFFTD EDTHLVKKFT
 80     LYVGDNWNKC DMVAIFLFIV GVTCRMLPSA FEAGRTVLAM DFMVFTLRLI
 85     HIFAIHKQLG PKIIVVERMM KDVFFFLFFL SVWLVAYGVT TQALLHPHDG
 90     RLEWIFRRVL YRPYLQIFGQ IPLDEIDEAR VNCSTHPLLL EDSPSCPSLY
 95     ANWLVILLLV TFLLVTNVLL MNLLIAMFSY TFQVVQGNAD MFWKFQRYNL
 100    IVEYHERPAL APPFILLSHL SLTLRRVFKK EAEHKREHLE RDLPDPLDQY
 105    VVTWETVQKE NFLSKMEKRR RDSEGEVLRK TAHRVDFIAK YLGGLREQEK
 110    RIKCLESQIN YCSVLVSSVA DVLAQGGGPR SSQHCGEGSQ LVAADHRGGI
 115    DGWEQPGAGQ PPSDT*
```

Figure 4
(Sheet 5 of 17)
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Figure 1 - Comparison of the amino acid sequences of mouse and human TRF1

```
mTrp   MCTTCSSCFGSILCLEDGWEISLCFGFIKFGGSGEEFGKFVKVFSSVAFSVLFELLLTEW  60
hTRF   MGDVQGFKPGSFGDALDEFELGLEKGEVNIGGSGEEFGKFVKVPSGVAPSVLFDLLLAEW  60
       **  *   **** *** *    *  *** ********** *   *:*** ****** :**

mTrp   ELFAFKLVVSLVGELEFFLAMFSWLRDVLKFGLVKAACSTGAWILTSALHVGLARHVGCAV  120
hTRF   ELFAFKLVVSLVGELQFFAMFSWLRDVLKKGLVKAACSTGAWILTSALFVGLARHVGCAV  120
       *********** *   ** :***************** ********** :**********

mTrp   RDHSLASTSTHIRVVAIGMASLDFILHRCLLDGVHQKEDTFIHYFADEGNIQGFLCFLDS  180
hTRF   RDHSLASTSTEVEVVAVGMASLGRVLHHILEAC--EDFPVHYPEDDGGSQGPLCSLDS  175
       **********  : **.*****  :*:  :: .:   **  :***  :*   ***.***

mTrp   NLSHFILVESGALGSGNDGLTELQLSLEKHISQCHTGYGGTSCIQIPVLCLLVNGDPNTL  240
hTRF   NLSHFILVEFGFFGHG-DGLTELFLKLLEHISLCHAGYGGTGSIEIPVLCLLVNGDPNTL  237
       *********.*   * *****  *  : *:*** :*.*****.  *:*************

mTrp   EHISHAVEQAAPWLILAGSGGIADVLAALVSCFHLLVFQVAEKQFREKFPSECFSWEAIV  300
hTRF   EHISHAVEQAAPWLILVGSGGIADVLAALVNCFHLLVFKVAEKQFKEKFPSKHFSWEDIV  297
       ****************.*************.*******:*******:*****  *****:*

mTrp   HWTELLQNIAAHFHLLTVYDFEQEGSEDLCTVILFALVKACKSHSQEAQDYLDELKLAVA  360
hTRF   FWTKLLQNITSHQHLLTVYDFEQEGSEELDTVILFALVKACKSHSQEPQDYLDELKLAVA  357
       :**:*****:::* ************:**  ****************** *********

mTrp   WDFVDIAKSEIFNGDVEWKSCDLEEVMTDALVSNHFDFVRLFVDSGADMAEFLTYGRLQQ  420
hTRF   WDFVDIAKSEIFNGDVEWKSCDLEEVMVDALVSNHIEFVRLFVDNGADVADFLTYGRLQE  417
       **************************** ******  ******* :*** .: :******* :

mTrp   LYHSVSFHSLLFELLQHFHEEGRLTLAGLGAQQARELFIGLFAFSLHEVSRVLKDFLHDA  480
hTRF   LYHSVSFHSLLFDLLQHKQEEAKLTLAGLGTQQARELFAGFFAFSLHEVSRVLKDFLQDA  477
       **:****  ***** :***:** ********* *:***** * : ***************:**

mTrp   CHGFYQDGH----RMEEKGFFKFFAGQKWLFELSHKSEDPWRDLFLWAVLQNRYEMATYF  536
hTRF   CHGFYQDGRFGDRRRAEKGFAKRPTGQKWLLDLNQKSENPWRDLFLWAVLQNRHEMATYF  537
       ********       : *** :**  *****  :*** ** :*** ***********:******

mTrp   WAMGREGVAAALAACKIIKEMSHLEKEAEVAFTMREAKYEQLALDLFSECYGNSEDRAFA  596
hTRF   WAMGQEGVAAALAACKILKEMSHLETEAEAKATREAKYERLALDLFSECYSNSEARAFA  597
       ****:********** :******* *** : ****** :********** *** ****
```

Figure 5
(Sheet 6 of 17)
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Classification and Secondary Structure Prediction of Membrane Proteins

http://azusa.proteome.bio.tuat.ac.jp/sosui/

```
Orientation of the N-terminus of      mTrp6:  IN
Number of transmembrane helices of    mTrp6:  6
Position of transmembrane helices of  mTrp6:  helix   begin    end
                                              1       732      754
                                              2       769      791
                                              3       807      829
                                              4       839      861
                                              5       870      892
                                              6       955      977


Orientation of the N-terminus of      hTrp6:  IN
Number of transmembrane helices of    hTrp6:  6
Position of transmembrane helices of  hTrp6:  helix   begin    end
                                              1       733      755
                                              2       770      792
                                              3       807      829
                                              4       843      865
                                              5       871      893
                                              6       955      977
```

Figure 6A
(Sheet 7 of 17)
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mTrp8_protein

Amino acid number 1158

mTrp8_protein

Amino acid number 1000
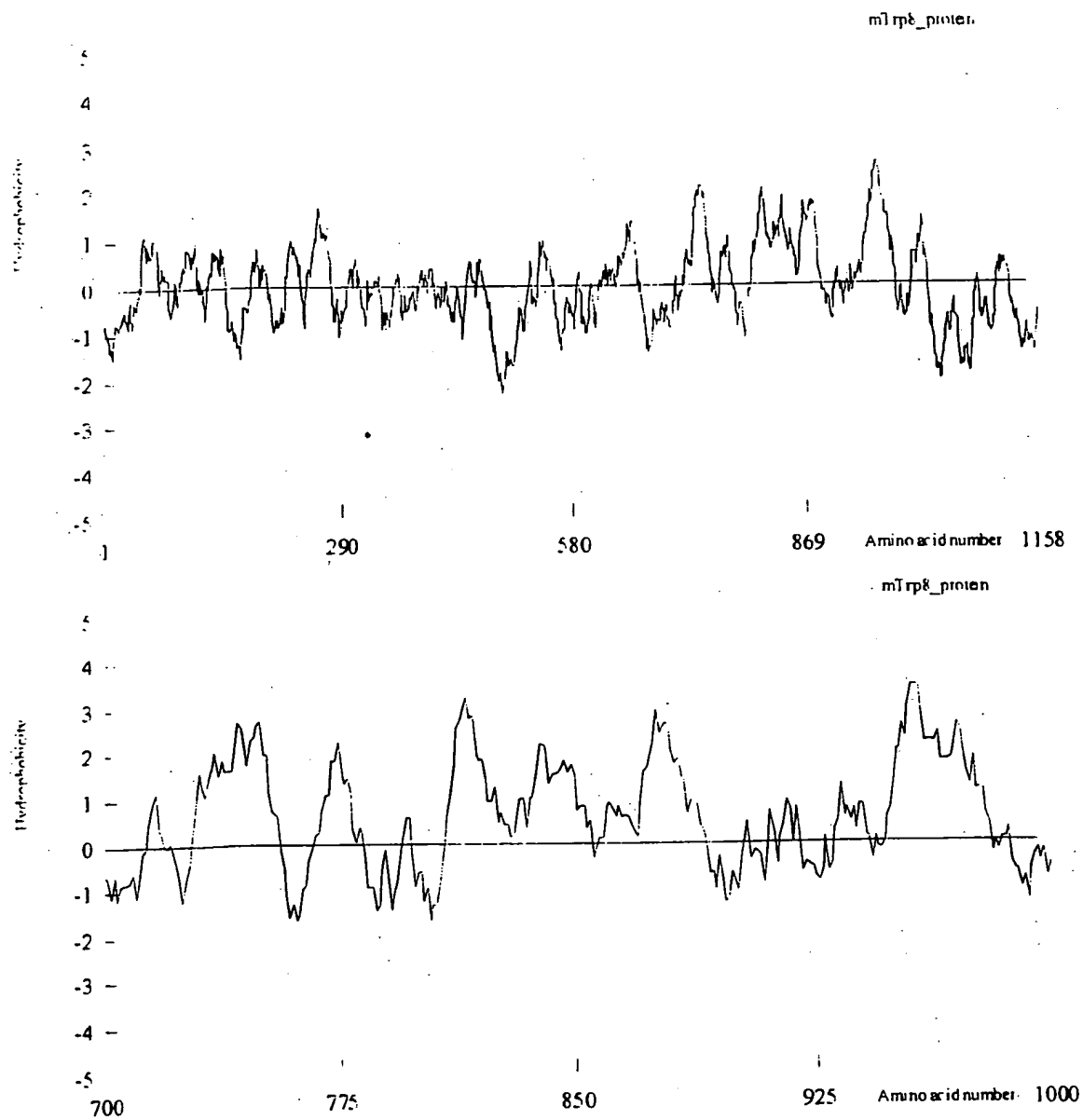
Figure 6B
(Sheet 8 of 17)
AP32911

hTrp8

Amino acid number

1   292   583   874   1165

hTrp8

Amino acid number

700   775   850   925   1000
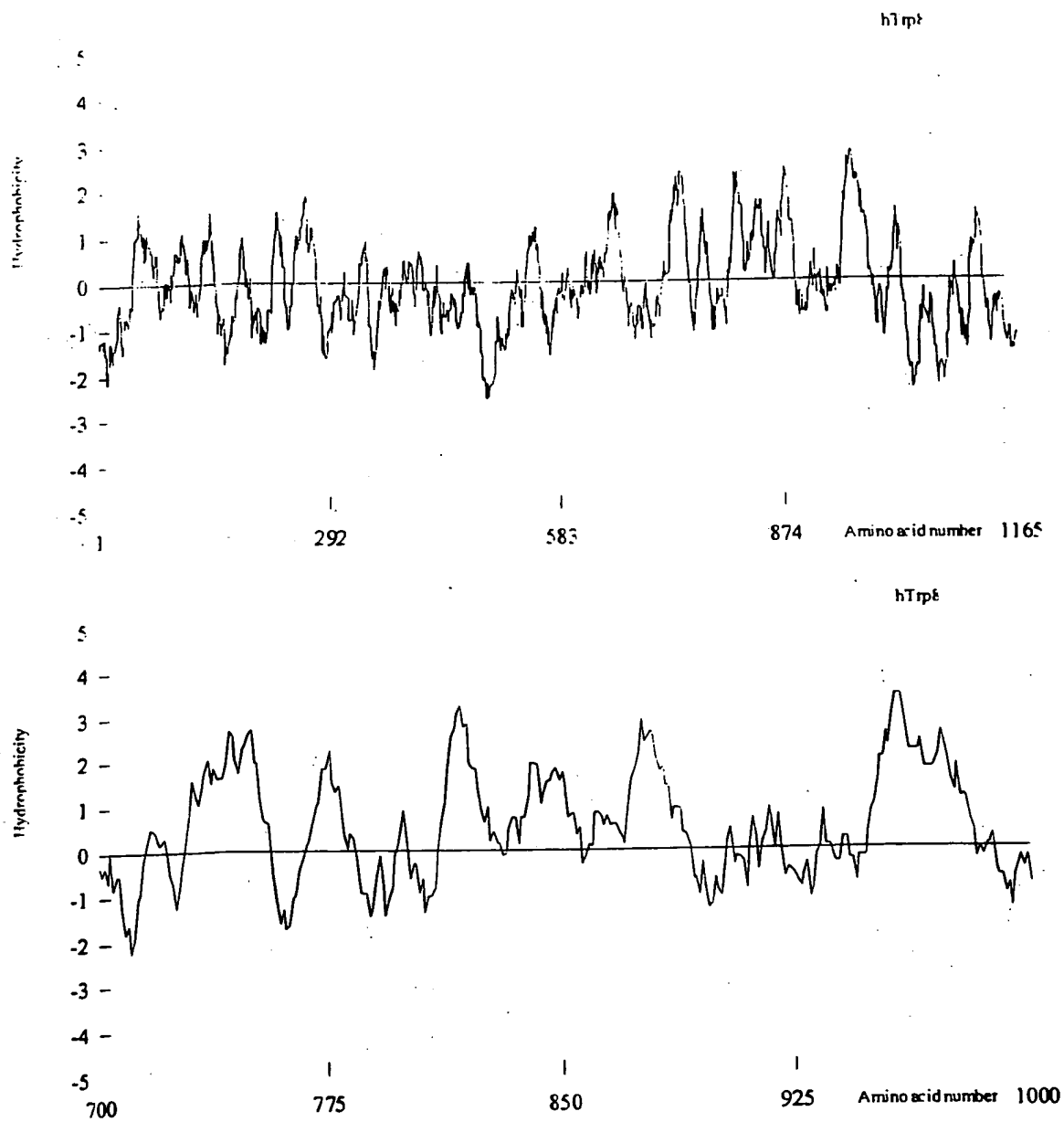
Figure 6C
(Sheet 9 of 17)
AP32911
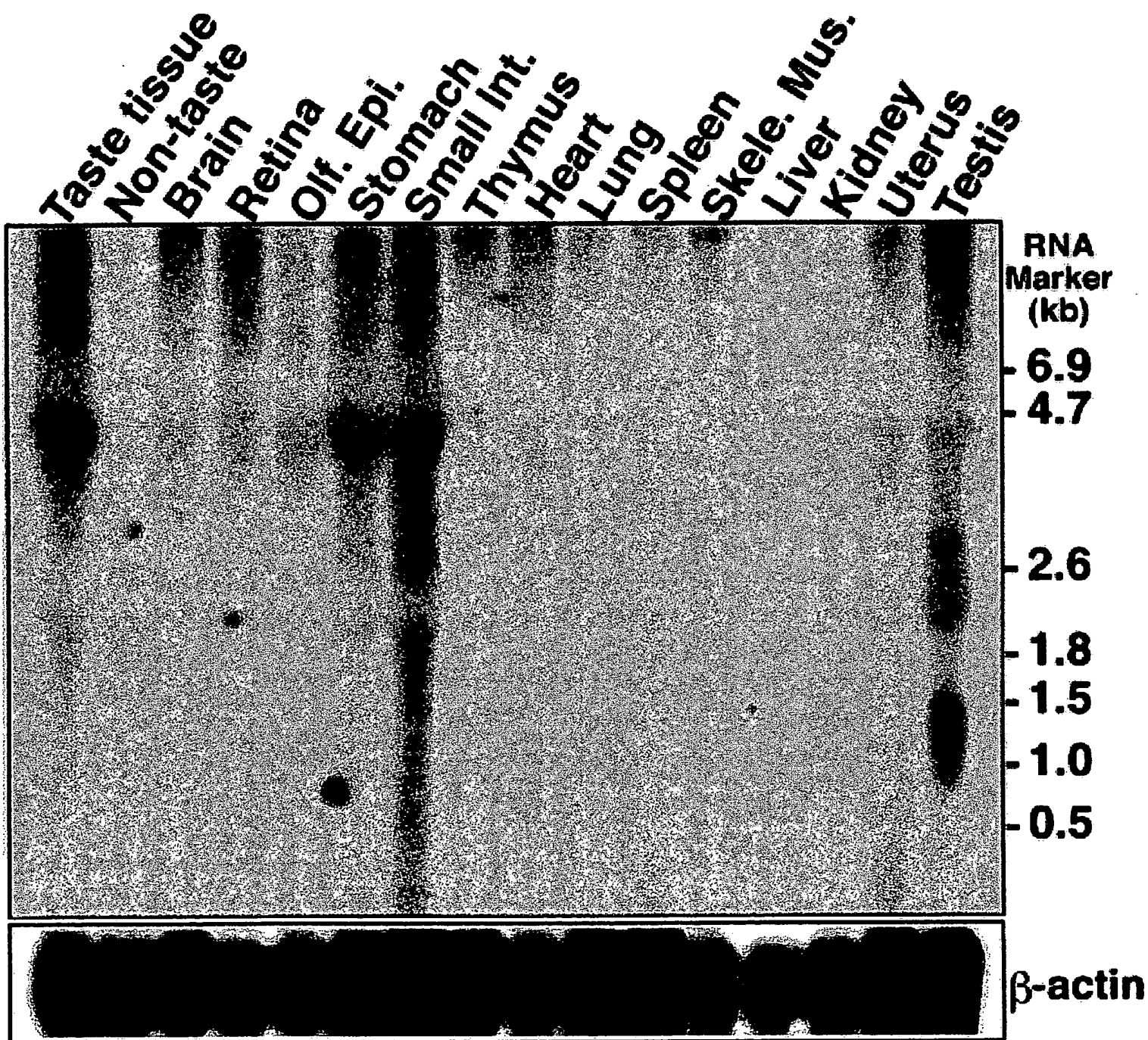
Figure 7
(Sheet 10 of 17)
AP32911
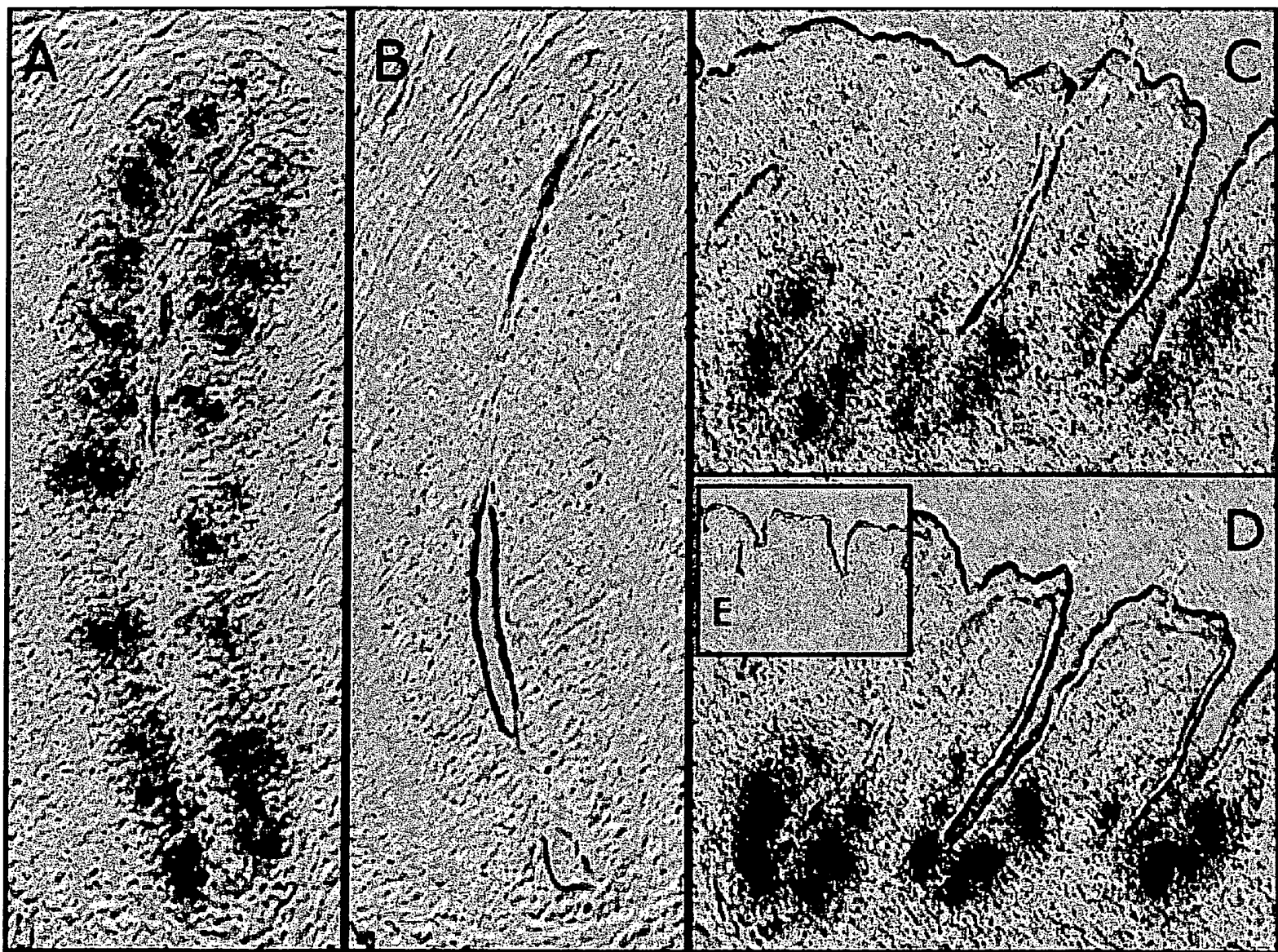
Figure 8
(Sheet 11 of 17)
AP32911
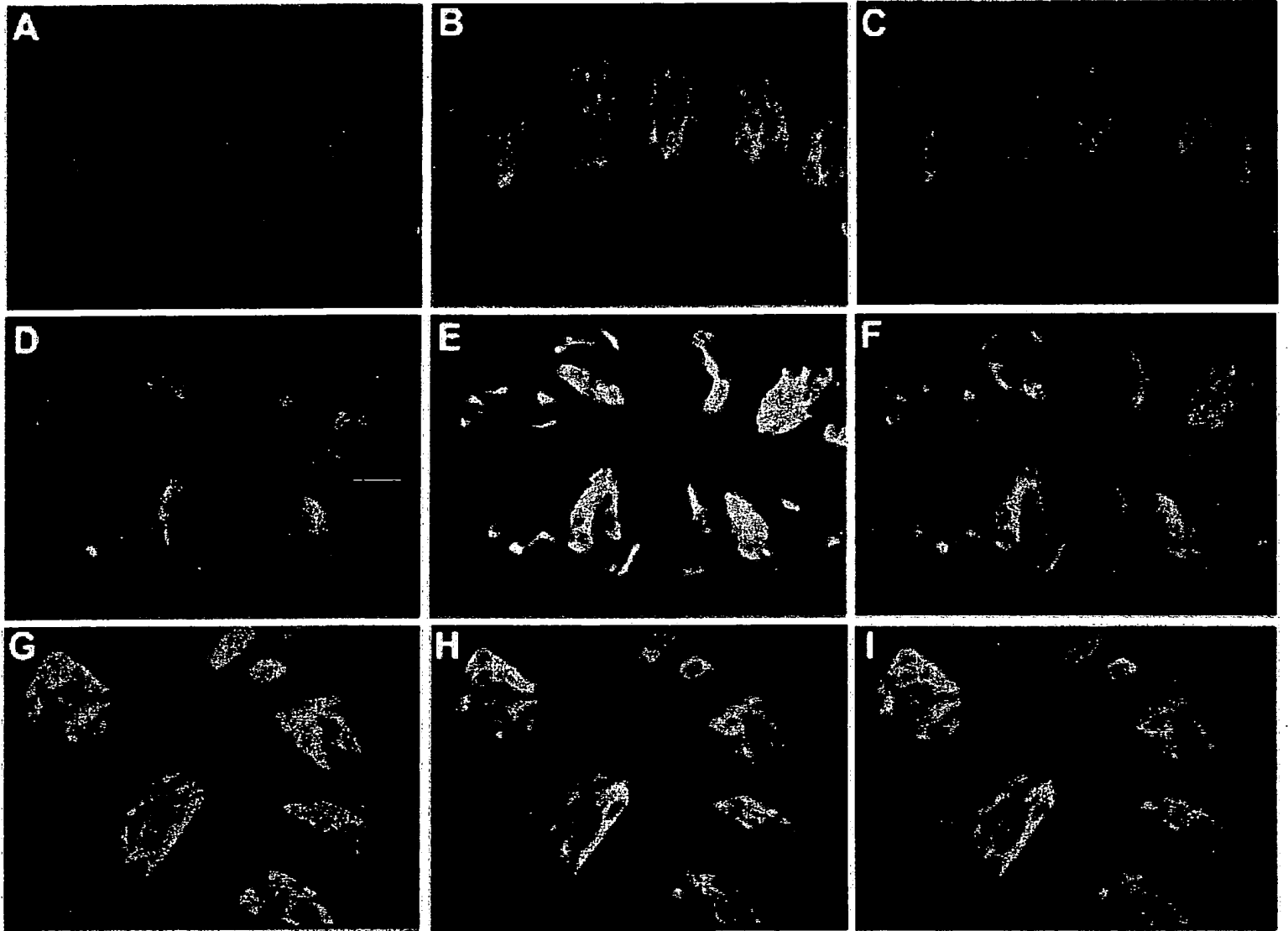
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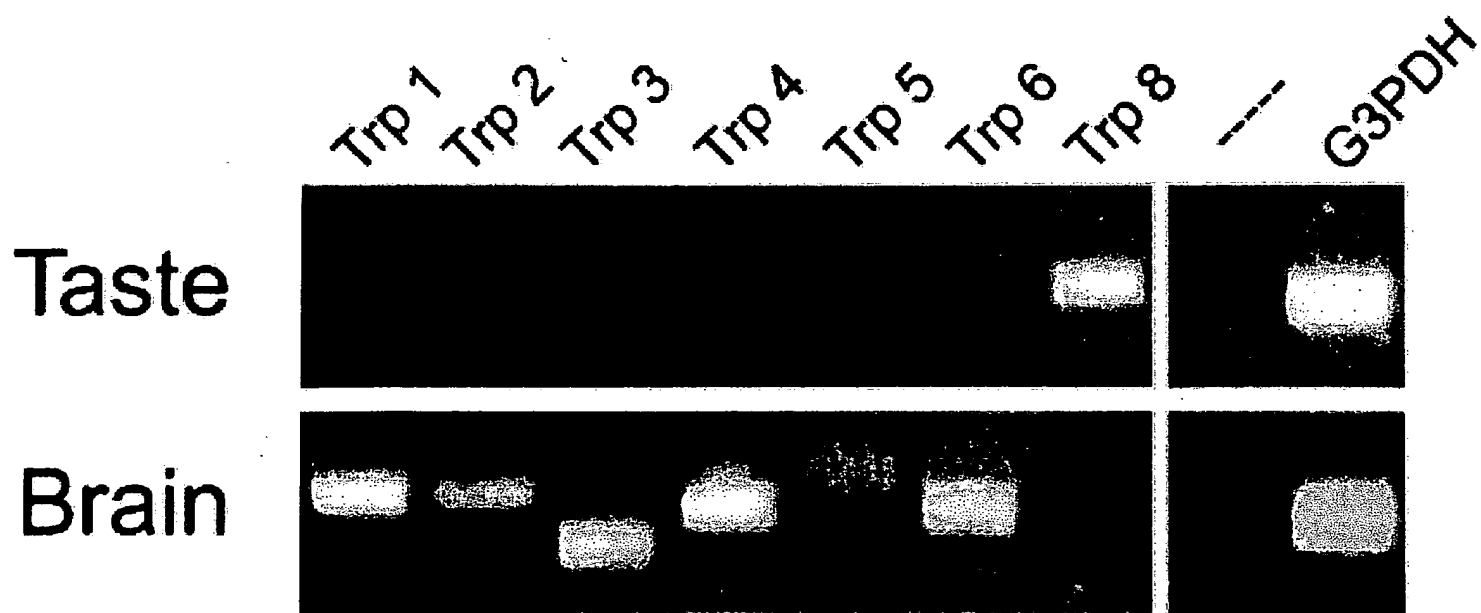(sheet 12 of 17)
AP 32911
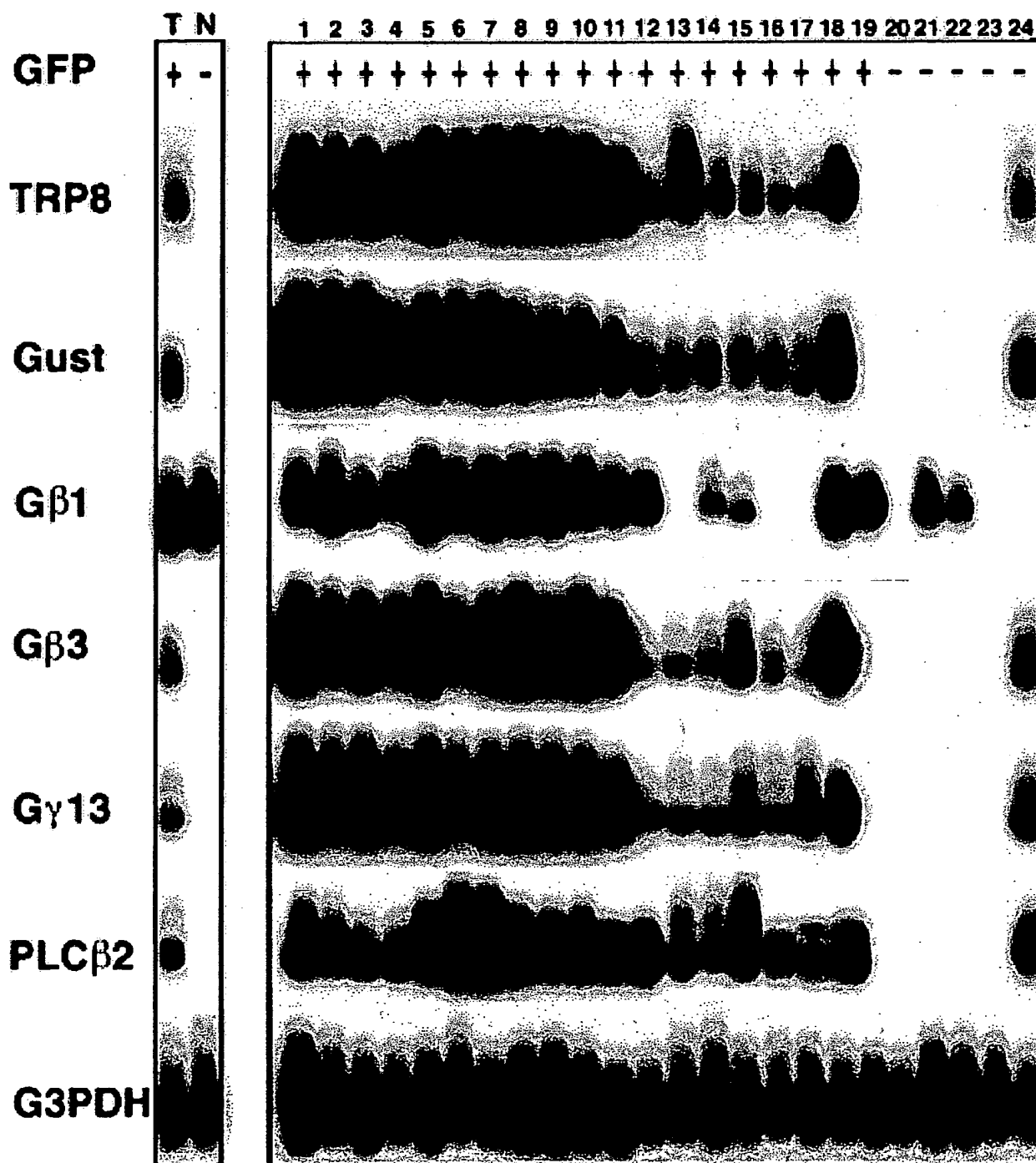
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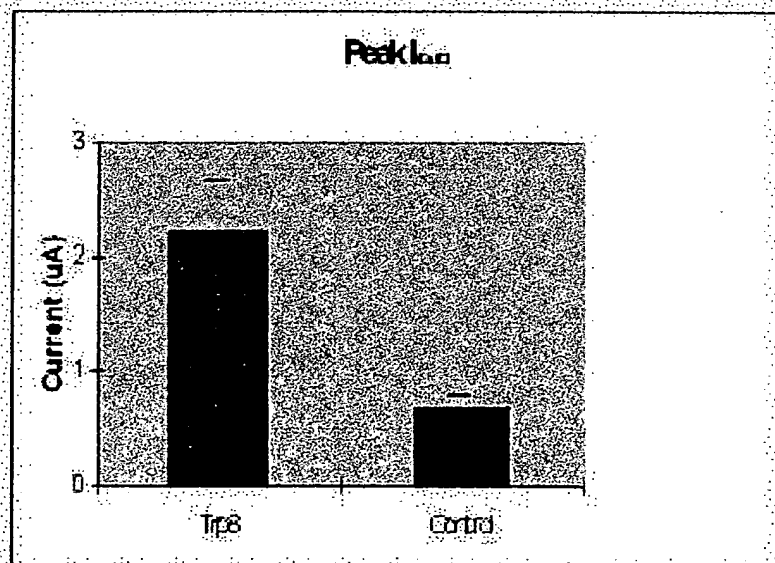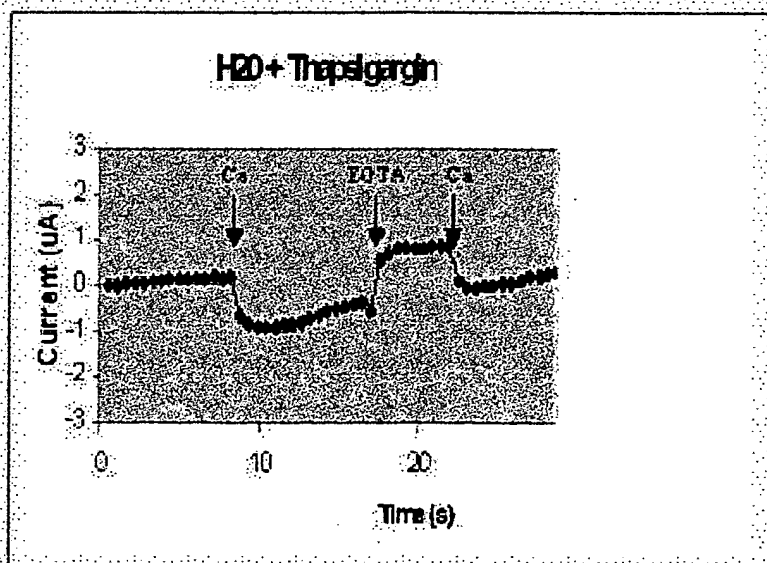(sheet 13 of 17)
AP32911

Figure II
(Sheet 14 of 17)
AP32911
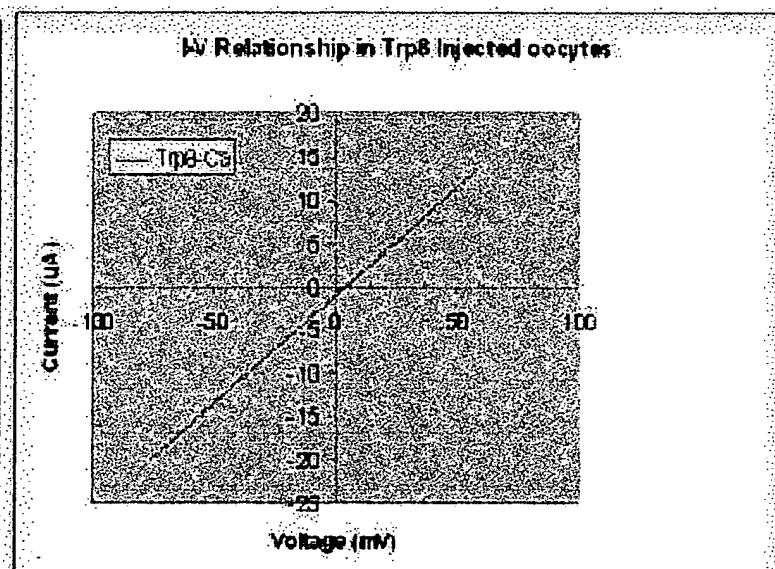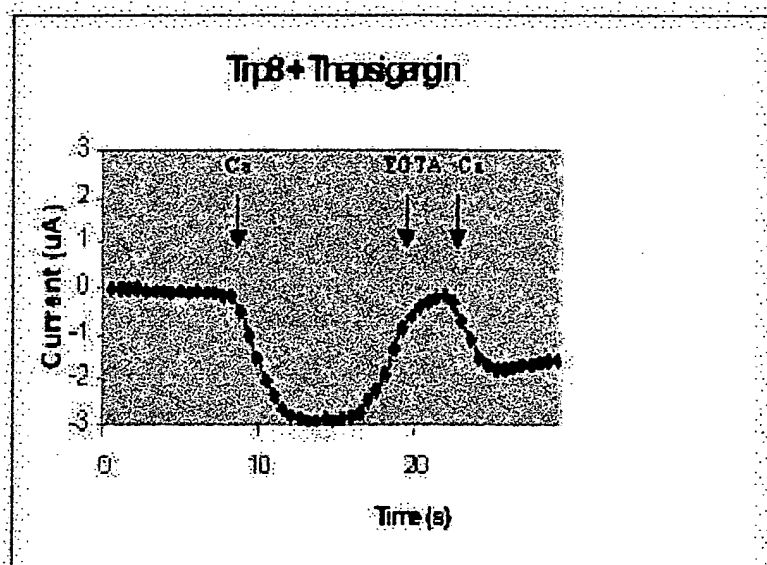
Figure 12
(sheet 15 of 17)
AP 32911
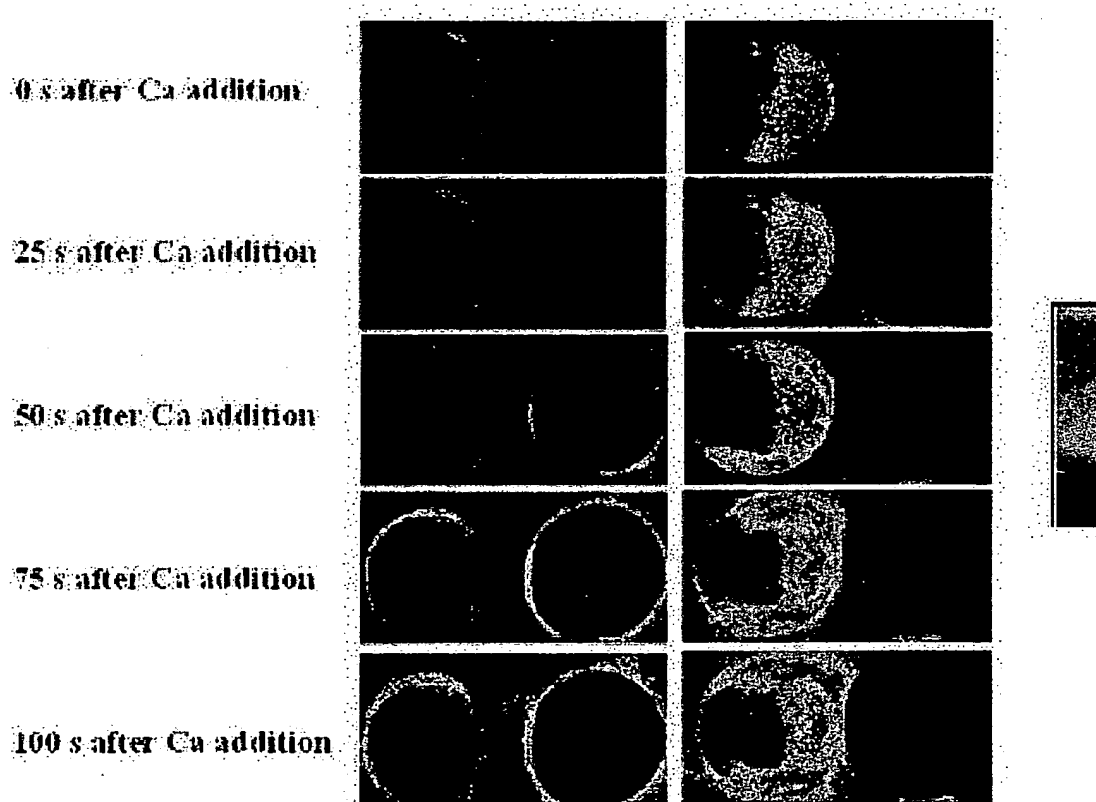
Figure 13
(Sheet 16 of 17)
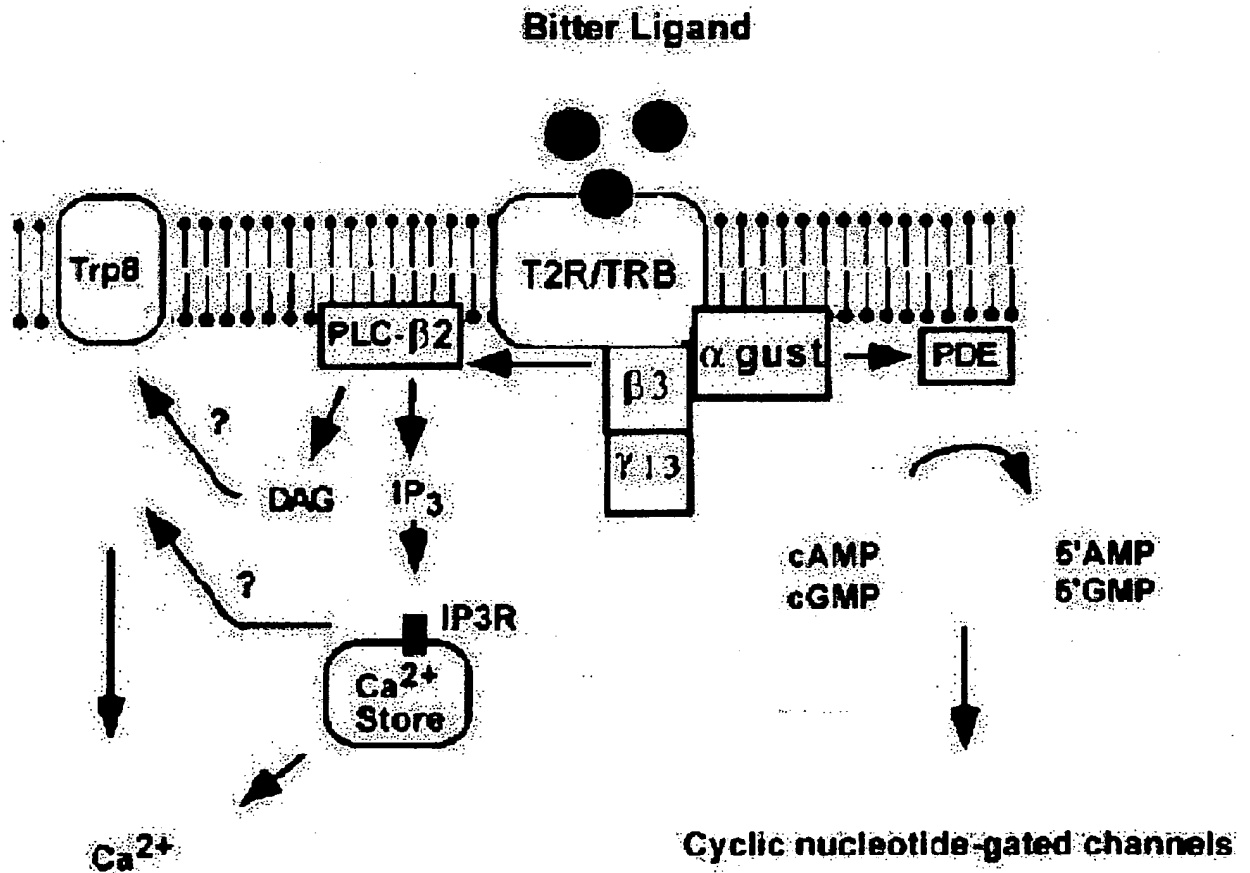AP32911

Transduction of Taste Stimuli

Bitter Ligand

Modified from Kinnamon, Neuron (2000) 25:507-510

Figure 14
(Sheet 17 of 17)
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